```
=============================================================
Sequence Listing could not be accepted due to errors.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2009; month=12; day=17; hr=11; min=8; sec=3; ms=26; ]
=============================================================


*************************************************************
Reviewer Comments:
<210>   10
<211>   519
<212>   PRT
<213>   Physcomitrella patens

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Met Thr Ser Thr Glu Asn Thr Ala Met Phe Thr Glu Asp Thr Ser Thr
1               5                   10                  15
Leu Asn Gly Ser Thr Glu Ala Asn His Ala Glu Phe Pro Leu Gly Glu
            20                  25                  30
Arg Pro Thr Ile Gly Pro Glu Pro Pro Val Asn Pro Phe His Glu Ser
            35                  40                  45
Ser Thr Trp Ser Ile Pro Gln Val Ile Lys Thr Ile Leu Leu Val Pro
        50                  55                  60
Leu Leu Val Ile Arg Leu Leu Ser Met Phe Ala Leu Met Met Leu Gly
65                  70                  75                  80
Tyr Ile Cys Val Lys Val Ala Met Ile Gly Cys Lys Asp Pro Leu Phe
                85                  90                  95
Lys Pro Phe Asn Pro Leu Arg Arg Leu Leu Leu Val Ser Val Arg Leu
            100                 105                 110
Ile Ala Arg Gly Val Met Val Ala Met Gly Tyr Tyr Tyr Ile Leu Val
            115                 120                 125
Lys Gly Lys Pro Ala His Arg Ser Val Ala Pro Ile Ile Val Ser Asn
        130                 135                 140
His Ile Gly Phe Val Asp Pro Ile Phe Val Phe Tyr Arg His Leu Pro
145                 150                 155                 160
Val Ile Val Ser Ala Lys Glu Ile Val Glu Met Pro Ile Ile Gly Met
                165                 170                 175
Phe Leu Gln Ala Leu Gln Ile Ile Pro Val Asp Arg Ile Asn Pro Ala
```

```
       180                    185                       190
```

Ser Arg His His Ala Ala Gly Asn Ile Arg Arg Arg Ala Met Asp Asn
```
        195                    200                       205
```
Glu Trp Pro His Val Met Leu Phe Pro Glu Gly Thr Thr Thr Asn Gly

In the above attachment, please delete the extra space between the bases.  This type of error is seen globally throughout the sequences in the sequence listing.

<210>  56
<211>  17752
<212>  DNA


<213>  Artificial sequence

<220>
<223>  Vector comprising genes coding for Physcomitrella patens Delta-6-elongase, Physcomitrella patens Delta-6-desaturase, and Phaeodactylum tricornutum Delta-5-desaturase

Invalid Line Length in Numeric Identifier <223>, The rules require that a line not exceed 72 characters in length.  This includes white spaces. Please check for similar errors and make necessary changes.
************************************************************

Validated By CRFValidator v 1.0.3

Application No:    10552013                Version No:         3.0


Input Set:


Output Set:


Started:         2009-11-23 16:16:35.058
Finished:        2009-11-23 16:16:53.988
Elapsed:         0 hr(s) 0 min(s) 18 sec(s) 930 ms
Total Warnings:  103
Total Errors:    202
No. of SeqIDs Defined:    148
Actual SeqID Count:       148

| Error code | | Error Description |
|---|---|---|
| W | 402 | Undefined organism found in <213>  in SEQ ID (1) |
| W | 402 | Undefined organism found in <213>  in SEQ ID (2) |
| E | 355 | Empty lines found between the amino acid numbering and the |
| E | 321 | No. of Bases conflict, this line has no nucleotides  SEQID (2) |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
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| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |
| E | 336 | Empty lines found between the proteins and the dna |

```
            Input Set:


            Output Set:



            Started:  2009-11-23 16:16:35.058
           Finished:  2009-11-23 16:16:53.988
            Elapsed:  0 hr(s) 0 min(s) 18 sec(s) 930 ms
     Total Warnings:  103
       Total Errors:  202
No. of SeqIDs Defined:  148
  Actual SeqID Count:  148
```

| Error code | Error Description |
| --- | --- |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides  SEQID (9) |
| E 300 | Invalid codon found   Met SEQID  (9)  POS: 920 |
| E 300 | Invalid codon found   Leu SEQID  (9)  POS: 923 |
| E 300 | Invalid codon found   Phe SEQID  (9)  POS: 926 |
| E 300 | Invalid codon found   Pro SEQID  (9)  POS: 929 |
| E 300 | Invalid codon found   Glu SEQID  (9)  POS: 932 |
| E 300 | Invalid codon found   Gly SEQID  (9)  POS: 935 |
| E 300 | Invalid codon found   Thr SEQID  (9)  POS: 938 |
| E 300 | Invalid codon found   Thr SEQID  (9)  POS: 941 |
| E 300 | Invalid codon found   Thr SEQID  (9)  POS: 944 |
| E 300 | Invalid codon found   Asn SEQID  (9)  POS: 947 |
| E 300 | Invalid codon found   Gly SEQID  (9)  POS: 950 |
| E 300 | Invalid codon found   Lys SEQID  (9)  POS: 953 |
| E 300 | Invalid codon found   Ala SEQID  (9)  POS: 956 |
| E 300 | Invalid codon found   Leu SEQID  (9)  POS: 959 |
| E 300 | Invalid codon found   Ile SEQID  (9)  POS: 962 |
| E 300 | Invalid codon found   Ser SEQID  (9)  POS: 965 |
| E 355 | Empty lines found between the amino acid numbering and the |
| E 321 | No. of Bases conflict, this line has no nucleotides  SEQID (11) |
| E 300 | Invalid codon found   Lys SEQID  (11)  POS: 961 |
| E 300 | Invalid codon found   Ala SEQID  (11)  POS: 964 |

```
              Input Set:


              Output Set:



             Started:   2009-11-23 16:16:35.058
            Finished:   2009-11-23 16:16:53.988
             Elapsed:   0 hr(s) 0 min(s) 18 sec(s) 930 ms
      Total Warnings:   103
        Total Errors:   202
 No. of SeqIDs Defined:  148
   Actual SeqID Count:   148


Error code        Error Description


E   300       Invalid codon found   Asn SEQID  (11)  POS: 967

E   300       Invalid codon found   Gln SEQID  (11)  POS: 970
               This error has occured more than 20 times, will not be displayed

W   402       Undefined organism found in <213>  in SEQ ID (16)

W   402       Undefined organism found in <213>  in SEQ ID (17)

W   402       Undefined organism found in <213>  in SEQ ID (18)

E   355       Empty lines found between the amino acid numbering and the

E   321       No. of Bases conflict, this line has no nucleotides  SEQID (18)

E   355       Empty lines found between the amino acid numbering and the

E   321       No. of Bases conflict, this line has no nucleotides  SEQID (18)

W   402       Undefined organism found in <213>  in SEQ ID (19)

W   402       Undefined organism found in <213>  in SEQ ID (28)

W   402       Undefined organism found in <213>  in SEQ ID (29)

W   402       Undefined organism found in <213>  in SEQ ID (30)

E   355       Empty lines found between the amino acid numbering and the

E   321       No. of Bases conflict, this line has no nucleotides  SEQID (30)

W   402       Undefined organism found in <213>  in SEQ ID (31)

W   402       Undefined organism found in <213>  in SEQ ID (32)

W   402       Undefined organism found in <213>  in SEQ ID (33)

W   402       Undefined organism found in <213>  in SEQ ID (36)

E   336       Empty lines found between the proteins and the dna

E   336       Empty lines found between the proteins and the dna

E   336       Empty lines found between the proteins and the dna
```

```
                Input Set:


                Output Set:



        Started:  2009-11-23 16:16:35.058
       Finished:  2009-11-23 16:16:53.988
        Elapsed:  0 hr(s) 0 min(s) 18 sec(s) 930 ms
 Total Warnings:  103
   Total Errors:  202
No. of SeqIDs Defined:  148
 Actual SeqID Count:  148
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| Error code | Error Description |
|---|---|
| E  336 | Empty lines found between the proteins and the dna<br> This error has occured more than 20 times, will not be displayed |
| W  402 | Undefined organism found in <213>  in SEQ ID (37) |
| E  355 | Empty lines found between the amino acid numbering and the |
| E  321 | No. of Bases conflict, this line has no nucleotides  SEQID (45) |
| E  355 | Empty lines found between the amino acid numbering and the |
| E  321 | No. of Bases conflict, this line has no nucleotides  SEQID (48) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (52) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (53) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (54) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (55) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (55) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (56) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (60) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (61) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (62) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (63) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (64) |

```
           Input Set:


           Output Set:



            Started:    2009-11-23 16:16:35.058
           Finished:    2009-11-23 16:16:53.988
            Elapsed:    0 hr(s) 0 min(s) 18 sec(s) 930 ms
     Total Warnings:    103
       Total Errors:    202
 No. of SeqIDs Defined:  148
   Actual SeqID Count:   148
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| Error code | Error Description |
|---|---|
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (65) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (65) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (66) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (67) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (68) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (71) |
| E  355 | Empty lines found between the amino acid numbering and the |
| E  321 | No. of Bases conflict, this line has no nucleotides  SEQID (71) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (75) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (75) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (76) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (76) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (77) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (78) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78) |
| W  213 | Artificial or Unknown found in <213>  in SEQ ID (79) This error has occured more than 20 times, will not be displayed |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79) |
| E  224 | <220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80) |

**Input Set:**


                    **Output Set:**



                    **Started:**  2009-11-23 16:16:35.058
                   **Finished:**  2009-11-23 16:16:53.988
                    **Elapsed:**  0 hr(s) 0 min(s) 18 sec(s) 930 ms
            **Total Warnings:**  103
              **Total Errors:**  202
      **No. of SeqIDs Defined:**  148
       **Actual SeqID Count:**  148

**Error code**      **Error Description**

E   224        <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (81)

E   224        <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (82)

E   224        <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (83)

E   224        <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (84)

E   224        <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (85)

E   224        <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (86)

E   224        <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (87)

E   224        <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (88)

E   224        <220>,<223> section required as <213> has Artificial sequence or
               Unknown in SEQID (89)
                This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110>   Renz, Andreas
        Sozer, Nursen
        Frentzen, Margit
        Bauer, Jorg
        Keith, Stobart
        Fraser, Thomas
        Lazarus, Colin M
        Qi, Baoxiu
        Abbadi, Amine
        Heinz, Ernst

<120>   NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY
        UNSATURATED FATTY ACIDS

<130>   13478-00002-US

<140>   10552013
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<150>   PCT/EP2004/003224
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<213>   Thraustochytrium

<220>
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<222>   (38)..(952)
<223>   LPAAT

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                                          1               5
gcc aag acc gcc gtg ggc ctc ctg acg ctg gcg cct gcg cgg ata gtg        103
Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
            10                  15                  20
ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc        151
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
        25                  30                  35
acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc        199
Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys

```
                40                       45                        50
gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc       247
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val
55                       60                       65                       70
tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg       295
Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala
                75                       80                       85
aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac       343
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His
                90                       95                      100
tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc       391
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val
        105                      110                      115
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc       439
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly
        120                      125                      130
ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct       487
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro
135                      140                      145                      150
cct cga gat tcg tcg agc gag aag cac cac gcg cag ccg ctt ctt gtg       535
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val
                155                      160                      165
ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag       583
Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys
                170                      175                      180
acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag       631
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu
        185                      190                      195
ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg       679
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser
        200                      205                      210
gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac       727
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His
215                      220                      225                      230
cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag       775
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu
                235                      240                      245
aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg       823
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala
                250                      255                      260
cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc       871
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu
        265                      270                      275
gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga       919
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly
        280                      285                      290
gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat gcgcgtccca       972
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu
295                      300                      305
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aaaaaaaaaa aaaaa                                                       1047


<210>  2
<211>  305
<212>  PRT
<213>  Thraustochytrium
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<400> 2

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1               5                   10                  15
Ala Pro Ala Arg Ile Val Phe Leu Val Thr Val Leu Gly Thr Tyr Gly
            20                  25                  30
Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
        35                  40                  45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
    50                  55                  60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65                  70                  75                  80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
                85                  90                  95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
                100                 105                 110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
        115                 120                 125
Ile Val Asp Arg Glu Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
    130                 135                 140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145                 150                 155                 160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
                165                 170                 175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val

                180                 185                 190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
        195                 200                 205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
    210                 215                 220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225                 230                 235                 240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
                245                 250                 255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
            260                 265                 270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
        275                 280                 285
Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
    290                 295                 300
Leu
305
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<210> 3
<211> 1701
<212> DNA
<213> Physcomitrella patens

<220>
<221> misc_feature
<223> LPAAT

<400> 3

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ggcacgaggg aaattggctt tctatgtggc cgtacttatt cgaggaggtc aacgaaacaa      60
aggtatgtct tattaatgaa aatgtctcca cacatgtatg ttgtttaggt atattctgtc     120
```

```
aactgaaaac ttgtttttaat ttttttcttaa attgaaattc tgtgcctgaa agccaactct     180
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tttgcaattt tcttttgctg ttaacctatt gattatgttg gaaccacaat acagacgctg     300
cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggttaattt catcctacag     360
ggatatggat gttgtaaagg tgattttttgc aggtgataaa gtacctaagg agaaccgtgt     420
gatggtcatg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat     480
tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc     540
cttgtttggt tgggcatttt acgttttttga gtttctgatg ctgcatagaa agtgggaagt     600
ggatgctccc gtcatcaaga catacattga cagttttcaa gataaaagag atcctctctg     660
gctagtcgtg tttcctgaag gcacagattt ttcgtaaggc tgaagtaccc atccatggct     720
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aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga     900
gagaaaggct atccggagct tgtcaatgtg cttcaacctc gcactcgtgg ctttgtgact     960
tgcctttctc aatcgcgctg ctctttggat gcagtttatg acctcactat agggtacaag    1020
aagcggtgtc ccttgttcat caacaatgta ttcggaaccg atccatcgga agtgcacatt    1080
cacattcgcc gaataccaat ttctgagatt cctcaatcag aagacggtat gacgcagtgg    1140
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aagctttatg tggctttcgc tagtttgctg ctcgcgttta gtacctattt tgattggaga    1380
cctaaaccgg tttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcgtt    1440
agttgtaatt ggtttgtttta ttccgattcc aaagctgagt ttaagggtga ggctcctctt    1500
taagctgatt tttgctatta attggctgct cccttgtttg tctgccgtaa attggcttta    1560
atacggttgt cttctgctga tgaacctcag tgcttcaaga cgatgtggcc ttttagcctt    1620
ctcctttacc catcttgacc agatgccaaa ctcgcaataa agcagatcaa taggtcgtgc    1680
cccaaaaaaa aaaaaaaaa a                                             1701
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<210>   4
<211>   714
<212>   DNA
<213>   Physcomitrella patens

<220>
<221>   CDS
<222>   (1)..(714)
<223>   LPAAT

<400>   4
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1               5                   10                  15

tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc        96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
            20                  25                  30

aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat       144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
        35                  40                  45

gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa       192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
    50                  55                  60

ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt       240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                  70                  75                  80

gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac       288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
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                   85                    90                    95
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             100                   105                   110
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca         384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
         115                   120                   125
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat         432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
     130                   135                   140
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca         480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                   150                   155                   160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg         528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
                 165                   170                   175
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta         576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
             180                   185                   190
ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc         624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
         195                   200                   205
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa         672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
     210                   215                   220
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Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
225                   230                   235


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             20                  25                  30
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
         35                  40                  45
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys
     50                  55                  60
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
65                  70                  75                  80
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
             85                  90                  95
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
             100                 105                 110
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
         115                 120                 125
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
     130                 135                 140
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
145                 150                 155                 160
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
             165                 170                 175
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Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
            180                 185                 190
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
        195                 200                 205
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys
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Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
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gataccctca caagtatgtc aaccccctctt ggtgtgacca aggaggtccg ttggtcgttg     300
tgttgcagct gatgactcag ttcatcaacc acatggaggt tgaatatttg ccggtcatga     360
agccaactgt gagagagatg aaataccctc atgaattcgc aagtagagtt cgcagcgaga     420
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ctc aac ggg ctc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa      96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu
            20                  25                  30
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc     144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
        35                  40                  45
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg     192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
    50                  55                  60
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg     240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65                  70                  75                  80
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc     288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile
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              85                    90                    95
ggc gtc aca gat ccc ttg ttt aag cct ttc aat ccg tgt cga cgg ttc          336
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